IN THE CLAIMS:

The claims as currently presented and under consideration, are presented below for the Examiner's convenience and to comply with 37 CFR §1.121. This listing of claims will replace all prior versions, and listings, of claims in the application:

1. **(Currently Amended)** A cutinase variant comprising ~~consisting essentially of~~ a substitution of the residue position corresponding to site 192 of the *Pseudomonas mendocina* cutinase set forth in SEQ ID NO:2, and wherein said variant has increased polyesterase activity ~~and/~~or enhanced thermostability, as compared to wild-type *Pseudomonas mendocina* cutinase.

Claims 2-18. (Cancelled)

19. (Currently Amended) The cutinase of claim 1, wherein said variant comprises the substitutions: Met at position 192, and further comprising the substitutions of Val at position 194, and Gly at position 219.

Claims 20-27. (Cancelled)

28. (Currently Amended) A cutinase variant consisting essentially of a substitution of the residue position corresponding to site 192, of the *Pseudomonas mendocina* cutinase set forth in SEQ ID NO:2, wherein said variant is more thermostable than wild-type *P. mendocina* cutinase, and wherein said cutinase variant has hydrolytic activity on polyester.

29. (Cancelled)

30. (Currently Amended) The cutinase variant of claim 28, wherein said variant further comprises a substitution of the amino acid residue at position 219 of *Pseudomonas mendocina* cutinase SEQ ID NO:2.

31. (Currently Amended) The cutinase variant of claim 1, wherein said variant further comprises a substitution of the amino acid residue at position 219 of *Pseudomonas mendocina* cutinase SEQ ID NO: 2.

32. (Cancelled)

33. (Previously Presented) The cutinase variant of claim 30, wherein the residue at position194 is substituted with Ala, His, Lys, Leu, Asn, Pro or Gly, and said residue at position 219 is substituted with Gly.

34. (Previously Presented) The cutinase variant of claim 1, wherein said variant comprises a substitution of the residue at position194 with one of Ala or His, and a substitution at 219 with Gly.

35. (Previously Presented) The cutinase variant of claim 1, wherein said variant comprises a substitution at position194 with Ile.

36. (Previously Presented) The cutinase variant of claim 1, wherein said variant comprises a substitution at position 194 with Lys or Leu and substitution at position 219 with Gly.

37. (Previously Presented) The cutinase variant of claim 1, wherein said variant comprises the substitution of Asn at position194.

38. (Previously Presented) The cutinase variant of claim 1, wherein said variant comprises the substitution of the residue at position 194 with Asn, Pro, or Ser, and substitution of the residue at position 219 with Gly.

39. (**Currently Amended**) A cutinase variant comprising~~consisting essentially of~~ a substitution of the residue position corresponding to site 194, of the *Pseudomonas mendocina* cutinase set forth in SEQ ID NO:2, and wherein said variant has increased polyesterase activity ~~and/~~or enhanced thermostability, as compared to wild-type *Pseudomonas mendocina* cutinase.

40. (Previously Presented) The cutinase variant of claim 39, wherein said variant further comprises the substitutions of Met at position 192, Val at position 194, and Ser at position 219.

41. (Previously Presented) The cutinase variant of claim 39, wherein said variant comprises a substitution of the residue at position194 with Ile, Leu, Asn, or Pro.

42. (Currently Amended) A cutinase variant consisting essentially of a substitution of the residue position corresponding to site 194 of the *Pseudomonas mendocina* cutinase set forth in SEQ ID NO:2, and wherein said variant is more thermostable than wild-type *P. mendocina* cutinase, and wherein said cutinase variant has hydrolytic activity on polyester.

43. (Previously Presented) The cutinase variant of claim 42, wherein said variant further comprises a substitution of the amino acid residue at position 219 of *Pseudomonas mendocina* cutinase SEQ ID NO:2.

44. (Previously Presented) The cutinase variant of claim 39, wherein said cutinase variant further comprises a substitution of the amino acid residue at position 219 of *Pseudomonas mendocina* cutinase SEQ ID NO:2.

45. (Previously Presented) The cutinase variant of claim 43, wherein said residue at position194 is substituted with Ala, His, Lys, Leu, Asn, Pro or Gly, and said residue at position 219 is substituted with Gly.

46. (Previously Presented) The cutinase variant of claim 39, wherein said variant comprises a substitution of the residue at position194 with Ala or His, and substitution at position 219 with Gly.

47. (Previously Presented) The cutinase variant of claim 39, wherein said variant comprises a substitution at position194 with Ile.

48. (Previously Presented) The cutinase variant of claim 39, wherein said variant comprises a substitution at position 194 with Lys or Leu, and substitution at position 219 with Gly.

49. (Currently Amended) The cutinase variant of claim 39, wherein said variant comprises the substitution of the residue at position 194 with Asn.

50. (Previously Presented) The cutinase variant of claim 39, wherein said variant comprises the substitution of the residue at position 194 with Asn, Pro, or Ser, and substitution of the residue at position 219 with Gly.